



## FIG 1

5'

GGC	GGA	GGC	GGA	GGC	GGA	GGG	CGA	GGG	GCG	GGG	AGC	GCC	GCC	TGG	AGC	GCG	GCA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
GGT	CAT	ATT	GAA	CAT	TCC	AGA	TAC	CTA	TCA	TTA	CTC	GAT	GCT	GTT	GAT	AAC	AGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AAG	ATG	GCT	TTG	AAC	TCA	GGG	TCA	CCA	CCA	GCT	ATT	GGA	CCT	TAC	TAT	GAA	AAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M	A	L	N	S	G	S	P	P	A	I	G	P	Y	Y	E	N	
CAT	GGA	TAC	CAA	CCG	GAA	AAC	CCC	TAT	CCC	GCA	CAG	CCC	ACT	GTG	GTC	CCC	ACT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
H	G	Y	Q	P	E	N	P	Y	P	A	Q	P	T	V	V	P	T
GTC	TAC	GAG	GTG	CAT	CCG	GCT	CAG	TAC	TAC	CCG	TCC	CCC	GTG	CCC	CAG	TAC	GCC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	Y	E	V	H	P	A	Q	Y	Y	P	S	P	V	P	Q	Y	A
CCG	AGG	GTC	CTG	ACG	CAG	GCT	TCC	AAC	CCC	GTC	GTC	TGC	ACG	CAG	CCC	AAA	TCC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	R	V	L	T	Q	A	S	N	P	V	V	C	T	Q	P	K	S
CCA	TCC	GGG	ACA	GTG	TGC	ACC	TCA	AAG	ACT	AAG	AAA	GCA	CTG	TGC	ATC	ACC	TTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	S	G	T	V	C	T	S	K	T	K	K	A	L	C	I	T	L
ACC	CTG	GGG	ACC	TTC	CTC	GTG	GGA	GCT	GCG	CTG	GCC	GCT	GGC	CTA	CTC	TGG	AAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	L	G	T	F	L	V	G	A	A	L	A	A	G	L	L	W	K
TTC	ATG	GGC	AGC	AAG	TGC	TCC	AAC	TCT	GGG	ATA	GAG	TGC	GAC	TCC	TCA	GGT	ACC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	M	G	S	K	C	S	N	S	G	I	E	C	D	S	S	G	T
TGC	ATC	AAC	CCC	TCT	AAC	TGG	TGT	GAT	GGC	GTG	TCA	CAC	TGC	CCC	GGC	GGG	GAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
C	I	N	P	S	N	W	C	D	G	V	S	H	C	P	G	G	E
GAC	GAG	AAT	CGG	TGT	GTT	CGC	CTC	TAC	GGA	CCA	AAC	TTC	ATC	CTT	CAG	GTG	TAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D	E	N	R	C	V	R	L	Y	G	P	N	F	I	L	Q	V	Y



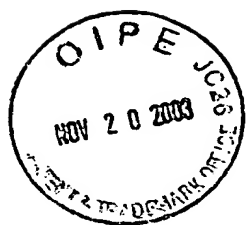
## FIG 1 (cont.)

TCA	TCT	605	CAG	AGG	AAG	614	TCC	TGG	CAC	623	CCT	GTG	TGC	632	CAA	GAC	GAC	641	TGG	AAC	GAG	650	AAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	S	Q	R	K	S	W	H	P	V	C	Q	D	D	W	N	E	N						
TAC	GGG	659	CGG	GCG	GCC	668	TGC	AGG	GAC	677	ATG	GGC	TAT	686	AAG	AAT	AAT	695	TTT	TAC	TCT	704	AGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y	G	R	A	A	C	R	D	M	G	Y	K	N	N	F	Y	S	S						
CAA	GGA	713	ATA	GTG	GAT	722	GAC	AGC	GGA	731	TCC	ACC	AGC	740	TTT	ATG	AAA	749	CTG	AAC	ACA	758	AGT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Q	G	I	V	D	D	S	G	S	T	S	F	M	K	L	N	T	S						
GCC	GGC	767	AAT	GTC	GAT	776	ATC	TAT	AAA	785	AAA	CTG	TAC	794	CAC	AGT	GAT	803	GCC	TGT	TCT	812	TCA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A	G	N	V	D	I	Y	K	K	L	Y	H	S	D	A	C	S	S						
AAA	GCA	821	GTG	GTT	TCT	830	TTA	CGC	TGT	839	ATA	GCC	TGC	848	GGG	GTC	AAC	857	TTG	AAC	TCA	866	AGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K	A	V	V	S	L	R	C	I	A	C	G	V	N	L	N	S	S						
CGC	CAG	875	AGC	AGG	ATT	884	GTG	GGC	GAG	893	AGC	GCG	CTC	902	CCG	GGG	GCC	911	TGG	CCC	TGG	920	TGG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
R	Q	S	R	I	V	G	G	E	S	A	L	P	G	A	W	P	W						
CAG	GTC	929	AGC	CTG	CAC	938	GTC	CAG	AAC	947	GTC	CAC	GTG	956	GGA	GGC	TCC	965	ATC	ATC	974	ACC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Q	V	S	L	H	V	Q	N	V	H	V	C	G	G	S	I	I	T						
CCC	GAG	983	TGG	ATC	GTG	992	ACA	GCC	GCC	1001	CAC	TGC	GTG	1010	GAA	AAA	CCT	1019	CTT	AAC	AAT	1028	CCA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	E	W	I	V	T	A	A	H	C	V	E	K	P	L	N	N	P						
TGG	CAT	1037	TGG	ACG	GCA	1046	TTT	GCG	GGG	1055	ATT	TTG	AGA	1064	CAA	TCT	TTC	1073	ATG	TTC	TAT	1082	GGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
W	H	W	T	A	F	A	G	I	L	R	Q	S	F	M	F	Y	G						
GCC	GGA	1091	TAC	CAA	GTA	1100	GAA	AAA	GTG	1109	ATT	TCT	CAT	1118	CCA	AAT	TAT	1127	GAC	TCC	AAG	1136	ACC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A	G	Y	Q	V	E	K	V	I	S	H	P	N	Y	D	S	K	T						
AAG	AAC	1145	AAT	GAC	ATT	1154	GCG	CTG	ATG	1163	AAG	CTG	CAG	1172	AAG	CCT	CTG	1181	ACT	TTC	AAC	1190	GAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K	N	N	D	I	A	L	M	K	L	Q	K	P	L	T	F	N	D						

## Replacement Sheet

FIG 1 (cont.)

1199				1208				1217				1226			1235			1244	
CTA	GTG	AAA	CCA	GTG	TGT	CTG	CCC	AAC	CCA	GGC	ATG	ATG	CTG	CAG	CCA	GAA	CAG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L	V	K	P	V	C	L	P	N	P	G	M	M	L	Q	P	E	Q		
1253				1262				1271				1280			1289			1298	
CTC	TGC	TGG	ATT	TCC	GGG	TGG	GGG	GCC	ACC	GAG	GAG	AAA	GGG	AAG	ACC	TCA	GAA		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L	C	W	I	S	G	W	G	A	T	E	E	K	G	K	T	S	E		
1307				1316				1325				1334			1343			1352	
GTG	CTG	AAC	GCT	GCC	AAG	GTG	CTT	CTC	ATT	GAG	ACA	CAG	AGA	TGC	AAC	AGC	AGA		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
V	L	N	A	A	K	V	L	L	I	E	T	Q	R	C	N	S	R		
1361				1370				1379				1388			1397			1406	
TAT	GTC	TAT	GAC	AAC	CTG	ATC	ACA	CCA	GCC	ATG	ATC	TGT	GCC	GGC	TTC	CTG	CAG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
Y	V	Y	D	N	L	I	T	P	A	M	I	C	A	G	F	L	Q		
1415				1424				1433				1442			1451			1460	
GGG	AAC	GTC	GAT	TCT	TGC	CAG	GGT	GAC	AGT	GGA	GGG	CCT	CTG	GTC	ACT	TCG	AAG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
G	N	V	D	S	C	Q	G	D	S	G	G	P	L	V	T	S	K		
1469				1478				1487				1496			1505			1514	
AAC	AAT	ATC	TGG	TGG	CTG	ATA	GGG	GAT	ACA	AGC	TGG	GGT	TCT	GGC	TGT	GCC	AAA		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
N	N	I	W	W	L	I	G	D	T	S	W	G	S	G	C	A	K		
1523				1532				1541				1550			1559			1568	
GCT	TAC	AGA	CCA	GGA	GTG	TAC	GGG	AAT	GTG	ATG	GTA	TTC	ACG	GAC	TGG	ATT	TAT		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
A	Y	R	P	G	V	Y	G	N	V	M	V	F	T	D	W	I	Y		
1577				1586				1595				1604			1613			1622	
CGA	CAA	ATG	AGG	GCA	GAC	GGC	TAA	TCC	ACA	TGG	TCT	TCG	TCC	TTG	ACG	TCG	TTT		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
R	Q	M	R	A	D	G	*												
1631				1640				1649				1658			1667			1676	
TAC	AAG	AAA	ACA	ATG	GGG	CTG	GTT	TTG	CTT	CCC	CGT	GCA	TGA	TTT	ACT	CTT	AGA		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
1685				1694				1703				1712			1721			1730	
GAT	GAT	TCA	GAG	GTC	ACT	TCA	TTT	TTA	TTA	AAC	AGT	GAA	CTT	GTC	TGG	CAA	AAA		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
1739																			
AAA	AAA	AAA	A	3'															



## FIG 2

A.

```
1  gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg
61  ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac
121 cggaaaaacc ctatcccgcg cagcccactg tgggtccccac tgtctacgag gtgcatccgg
181 ctcagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca
241 acccgcgtcg ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta
301 agaaagcact gtgcatcacc ttgaccctgg ggaccttccg cgtgggagct gcgctggccg
361 ctggcctact ctggaagttc atgggcagca agtgctccaa ctctgggata gagtgcgact
421 cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg
481 gggaggacga gaatcgggtg gttcgcctct acggaccaa cttcatcctt cagatgtact
541 catctcagag gaagtccctg caccctgtgt gccaaagcga ctggaacgag aactacgggc
601 gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg
661 atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct
721 ataaaaaact gtaccacagt gatgcctgtt cttcaaaagc agtggtttct ttacgctgtt
781 tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtgggc ggtgagagcg
841 cgctcccggg ggcctggccc tggcaggtca gcctgcacgt ccagaacgtc cacgtgtgcg
901 gaggtccat catcaccccc gagtggatcg tgacagccgc ccactgcgtg gaaaaacctc
961 ttaacaatcc atggcattgg acggcatttg cggggatttt gagacaatct ttcattgtct
1021 atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca
1081 agaacaatga cattgcgctg atgaagctgc agaagcctct gactttcaac gacctagtga
1141 aaccagtgtg tctgcccac ccaggcatga tgctgcagcc agaacagctc tgctggattt
1201 ccgggtgggg ggccaccgag gagaaaggga agacctcaga agtgctgaac gctgccaagg
1261 tgctttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac
1321 cagccatgat ctgtgccggc ttctcgagg ggaacgtcga ttcttgccag ggtgacagtg
1381 gagggcctct ggtcacttcg aacaacaata tctggtggct gataggggat acaagctggg
1441 gttctggctg tgccaaagct tacagaccag gagtgtacgg gaatgtgatg gtattcacgg
1501 actggattta tcgacaaatg aaggcaaacg gctaattccac atggtcttcg tccttgacgt
1561 cgtttttaca gaaaacaatg gggctggttt tgcttccccg tgcatgattt actcttagag
1621 atgattcaga ggtcacttca tttttattaa acagtgaact tgtctggctt tggcactctc
1681 tgccatactg tgcaggctgc agtggctccc ctgcccagcc tgctctccct aacccttgtt
1741 ccgcaagggg tgatggccgg ctggttgtgg gcactggcgg tcaattgtgg aagggaagg
1801 gttggaggct gccccatttg agatcttccg gctgagtcct ttccaggggc caattttgga
1861 tgagcatgga gctgtcactt ctgagctgct ggatgacttg agatgaaaaa ggagagacat
1921 ggaaagggag acagccaggt ggcacctgca gcggctgccc tctggggcca cttggtagtg
1981 tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagccctg
2041 gatggtggcc agaaataaag ggaccagccc ttcatgggtg gtgacgtggt agtcacttgt
2101 aaggggaaca gaaacatttt tgttcttatg gggtgagaat atagacagtg cccttggtgc
2161 gagggaagca attgaaaagg aacttgccct gagcactcct ggtgcaggtc tccacctgca
2221 cattgggtgg ggctcctggg agggagactc agccttccct ctcactctcc ctgaccctgc
2281 tcctagcacc ctggagagtg aatgccctt ggtccctggc agggcgccaa gtttgacc
2341 atgtcgccct cttcaggcct gatagtcat ggaaattgag gtccatgggg gaaatcaagg
2401 atgctcagtt taaggtaac tgtttccatg ttatgtttct acacattgat ggtggtgacc
2461 ctgagttcaa agccatctt
```

## B. ORF AMINO ACID SEQUENCE

MALNSGSPPAIGPYENHGYQPENPYPAQPTVVPTVYEVHPAQYYPSVPVQYAPRVL  
TQASNPVVCTQPKSPSGTVCTSKTKKALCITLTLGTFLVGAALAAGLLWKFMGSKCS  
NSGIECDSSGTCINPSNWCdGVSHCPGGEDENRCVRLYGPNFILQMYSSQRKSWHPV  
CQDDWNENYGRAACRDMGYKNNFYSSQGIVDDSGSTSFMKLNTSAGNVDIYKKLYHS  
DACSSKAVVSLRCLACGVNLNSSRQSRIVGGESALPGAWPWQVSLHVQNWHVCGGSI  
ITPEWIVTAAHCVEKPLNPNWHWTAFAGILRQSFMYGAGYQVQKVISHPNYDSKTK  
NNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWGATEEEKGKTSEVLNA  
AKVLLIETQRCNSRYVDNLITPAMICAGFLQGNVDSCQGDSSGGLVTSNNNIWWLI  
GDTSWGSGCAKAYRPGVYGNVMVFTDWIYRQMKANG



FIG 3

1	15 16	30 31	45 46	60 61	75 76	90
GTC1	MALNSGSPPAIGPY ENHGYQPENPYPAQ	TVVPTVVEVHFAQY PSPVQYAPRVLTA	SNPVVCTQPKSPSGT VCTSKTKKALCITLT			90
TMPRSS2	MALNSGSPPAIGPY ENHGYQPENPYPAQ	TVVPTVVEVHFAQY PSPVQYAPRVLTA	SNPVVCTQPKSPSGT VCTSKTKKALCITLT			90
91	105 106	120 121	135 136	150 151	165 166	180
GTC1	LGTFLVGAALAAAGLL WKFMGSKCSNSGIEC	DSSGTCINPSNWCDG VSHCPGGEDENRCVR	LYGPNFILOMYSSQR KSWHPVCQDDWNENY			180
TMPRSS2	LGTFLVGAALAAAGLL WKFMGSKCSNSGIEC	DSSGTCINPSNWCDG VSHCPGGEDENRCVR	LYGPNFILOMYSSQR KSWHPVCQDDWNENY			180
181	195 196	210 211	225 226	240 241	255 256	270
GTC1	GRAACRDMGYKNNFY SSQGIIVDDSGSTSM	KLNTSAGNVDIYKKL YHSDACSSKAVVSLR	CLACGVNLNSSRQSR IVGGESALPGAWPWQ			270
TMPRSS2	GRAACRDMGYKNNFY SSQGIIVDDSGSTSM	KLNTSAGNVDIYKKL YHSDACSSKAVVSLR	CLACGVNLNSSRQSR IVGGESALPGAWPWQ			270
271	285 286	300 301	315 316	330 331	345 346	360
GTC1	VSLHVQNVHVCGGSI ITPEWIVTAAHCVEK	PLNNPWHWTAFAGIL RQSEMFYAGYQVQK	VISHPNYDSKTKNND IALMKLQKPLTFNDL			360
TMPRSS2	VSLHVQNVHVCGGSI ITPEWIVTAAHCVEK	PLNNPWHWTAFAGIL RQSEMFYAGYQVQK	VISHPNYDSKTKNND IALMKLQKPLTFNDL			360
361	375 376	390 391	405 406	420 421	435 436	450
GTC1	VKPVCLPNPGMMLQP EQLCWISGWGATEEK	GKTSEVLNAAKVILLI ETQRCNSRYVVDNLI	TPAMICAGFLQGNVD SCQGDSGGPLVTSN			450
TMPRSS2	VKPVCLPNPGMMLQP EQLCWISGWGATEEK	GKTSEVLNAAKVILLI ETQRCNSRYVVDNLI	TPAMICAGFLQGNVD SCQGDSGGPLVTSN			450



FIG 3 cont.

451	465	466	480	481	
GTC1	NIWLLIGDTSWGSGC	AKAYRPGVYGNVMVF	TDWIYRQMPADG		492
TPRSS2	NIWLLIGDTSWGSGC	AKAYRPGVYGNVMVF	TDWIYRQMPANG		492

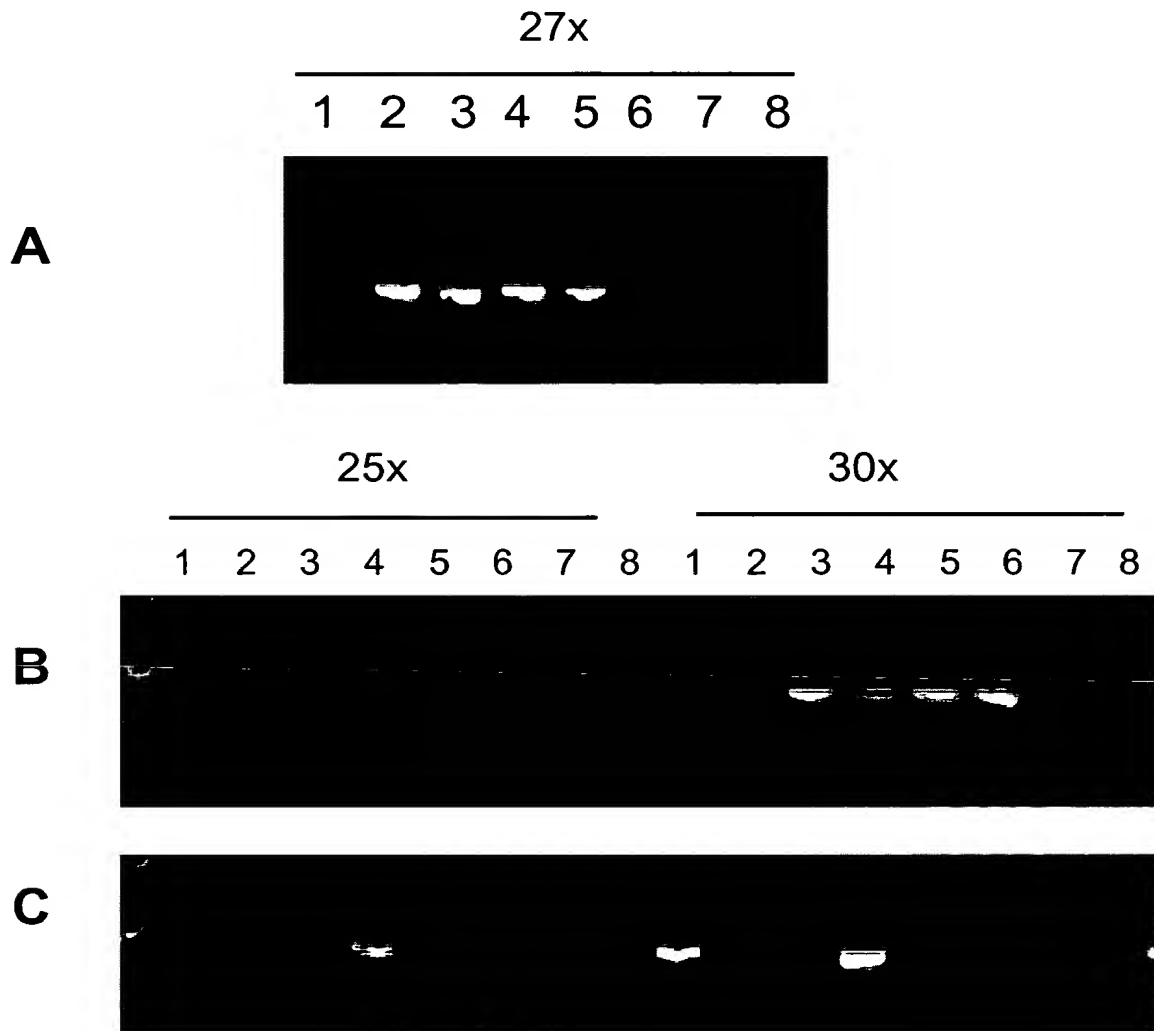


## FIG 4

GATCTTCCTGCTGAGTCCTTTCCAGGGGCCAATTTTGGATGAGCATGGAGCTGTCAC  
CTCTCAGCTGCTGGATGACTTGAGATGAAAAAGGAGAGACATGGAAAGGGAGACAGC  
CAGGTGGCACCTGCAGCGGCTGCCCTCTGGGGCCACTTGGTAGTGTCCCCAGCCTAC  
CTCTCCACAAGGGGATTTTGCTGATGGGTTCTTANAGCCTTAGCAGCCCTGGATGGT  
GGCCAGAAATAAAGGGACCAGCCCTTCATGGGTGGTGACGTGGTANTCACTTGTAAG  
GGGAACAGAAACATTTTGTTCCTTATGGGGTGAGAATATAGACAGTGCCCTTGGTGC  
GAGGGAAGCAATTGAAAAGGAACTTGCCCTGAGCACTCCTGGTGCA



FIG. 5

**A**

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

**B**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**C**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus





FIG. 6

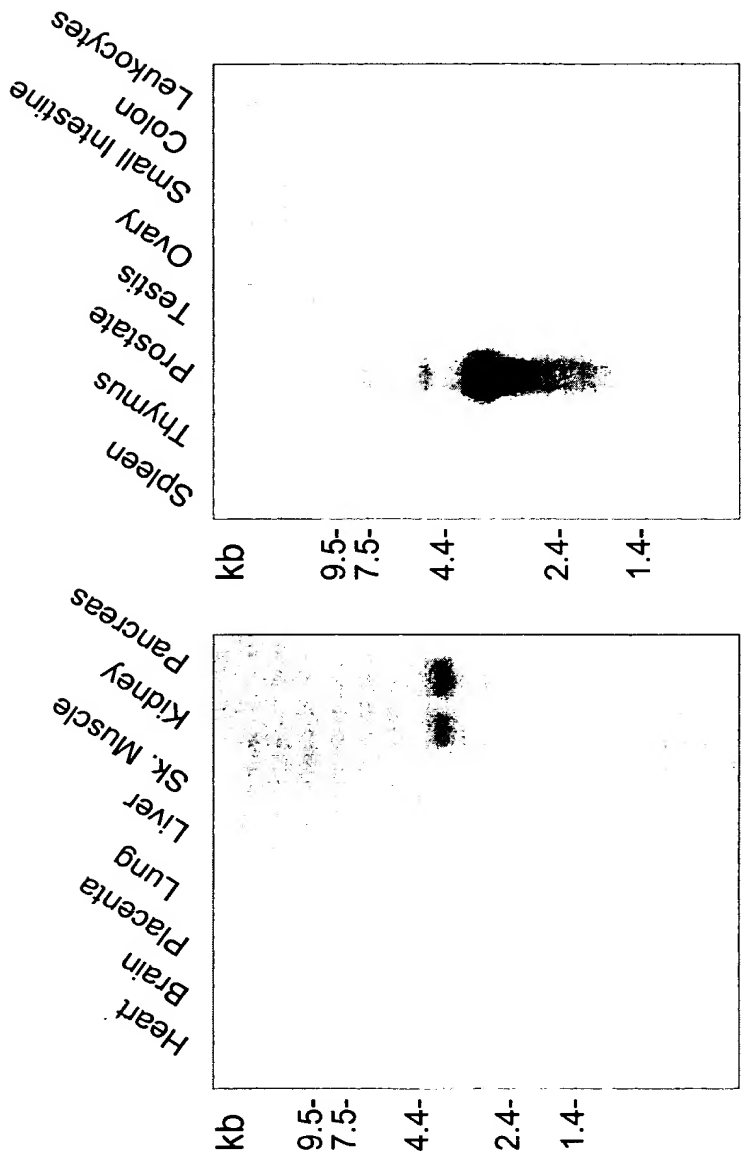
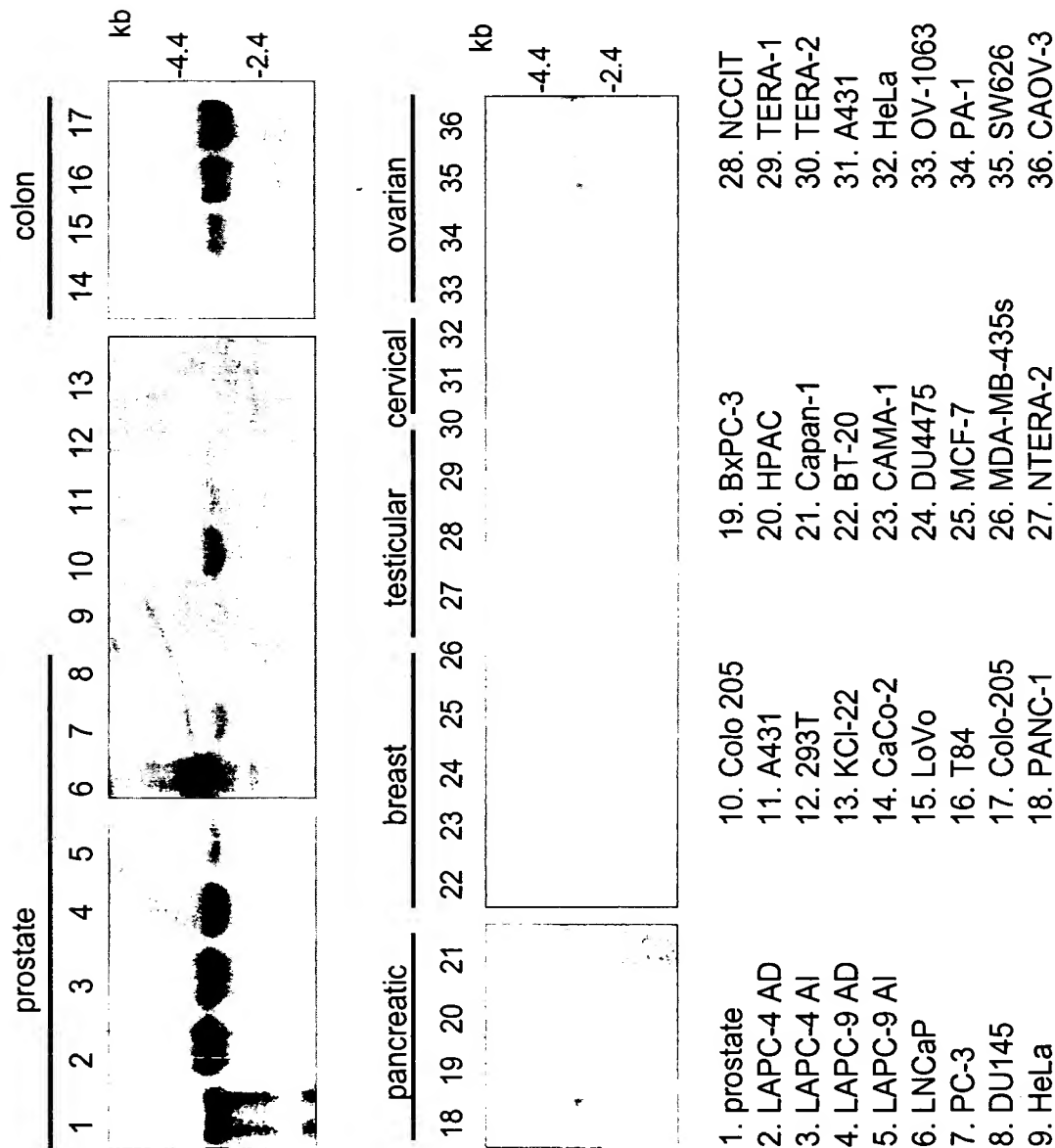


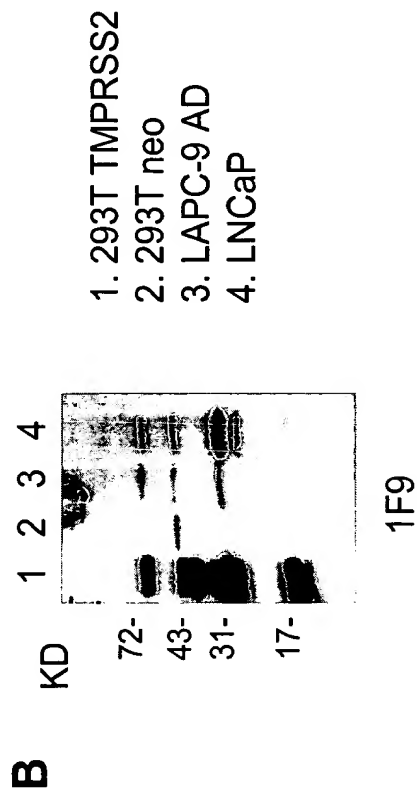
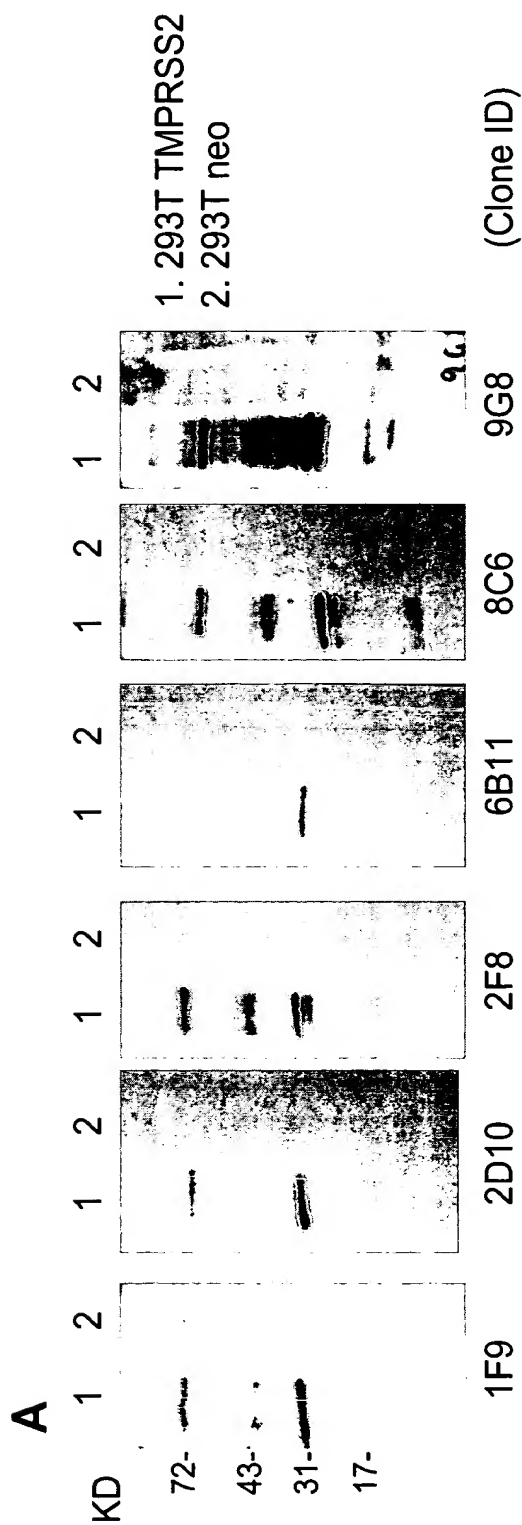


FIG. 7





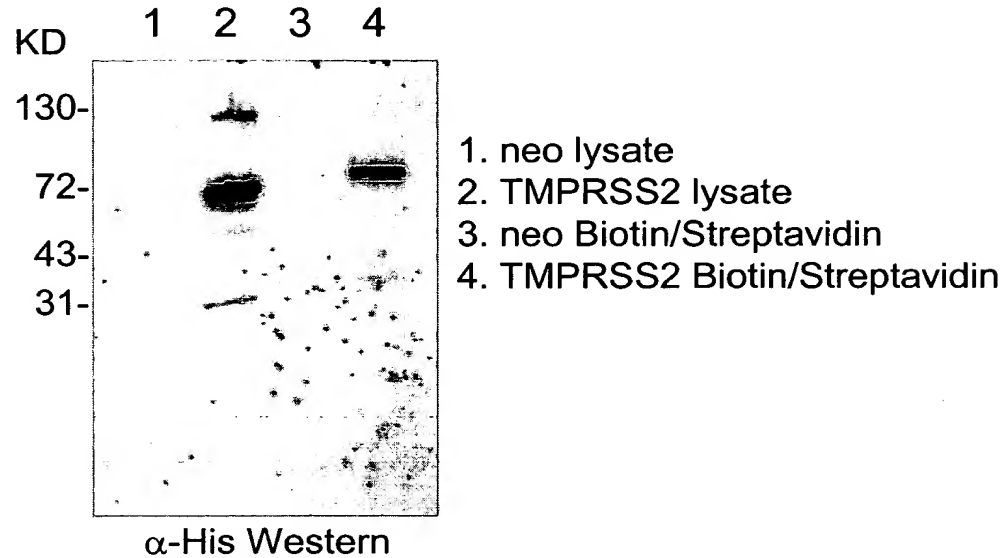
**FIG. 8**





## FIG. 9

### A. In transfected 293T cells:



### B. In prostate cancer cells:

